Biochemistry

BINDING PROPERTIES OF THE CAENORHABDITIS ELEGANS RECEPTOR ASSOCIATED PROTEIN

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Caenorhabditis elegans (*C. elegans*), a nematode, was investigated as a possible model system in which to study the structure and function of cell surface receptor proteins in the low density lipoprotein receptor (LDLR) family. LDLR family members have a diversity of functions and have been implicated in the pathology of cardiovascular disease and Alzheimer's disease. To date, genetic homologues of LDLR family receptor proteins LRP and megalin and a receptor-binding protein, RAP, have all been identified in *C. elegans*. The predicted protein product of the *C. elegans* RAP gene has 30% sequence identity with the human RAP protein. In order to examine the efficacy of C. elegans as a model system for in vivo and gene knockout studies of the RAP/ LDLR family system, the binding properties of the *C. elegans* RAP were studied.

Immunofluorescent (IF) staining of whole mounts of *C. elegans* nematodes exposed to human RAP were found to display unique and reproducible fluorescence patterns, most significantly punctuate lines in the anterior region. Previous IF studies have already established that the expression of *C. elegans* megalin is localized in punctuate lines, and our study confirmed this observation. Some experiments show C. elegans LRP and human RAP co-localize, suggesting that nematode LRP is similar enough in structure to the human receptor that it will recognize at least one human receptor ligand.

The gene for *C. elegans* RAP was cloned into a GST-fusion protein vector in collaboration with D. K. Strickland at the University of Maryland Medical School, Baltimore. Preliminary solid phase binding studies of the expressed nematode RAP-GST fusion protein indicate that this protein binds to human LRP, albeit fairly weakly.

These results suggest that *C. elegans* may be a viable model system in which to investigate the structure and function of this diverse family of cell surface receptors.